

REMARKS

Claims 1-2, 6-14, 16 and 28-33 are pending, upon entry of the amendment submitted above. Favorable reconsideration is respectfully requested.

Applicants would like to thank Examiner Fronda for the helpful and courteous discussion held with their representative on January 18, 2005 and a subsequent telephone discussion. During the discussions, the amendments presented above were discussed. Applicants' representative also presented the Examiner with the results of the BLASTN search attached hereto. As noted on the Interview Summary form, the "BLASTN search results-shows significant alignments to coryneform bacterium citrate synthases."

At the discussion, the Examiner indicated that the amendments appear to place the application in condition for allowance, and that a final decision would be made after a written response was filed. The following remarks expand on the discussion with the Examiner.

The rejection under 35 U.S.C. §112, first paragraph, is believed to be obviated by the amendments submitted above.

Claim 1 has been amended to specify a citrate synthase gene obtained from *Corynebacterium glutamicum* or *Brevibacterium lactofermentum*. Claim 16 has been amended to specify that the citrate synthase gene is obtained from corynebacterium chromosomal DNA by the polymerase chain reaction using oligonucleotide primers of SEQ ID NO: 1 and SEQ ID NO: 2.

In view of those amendments, the results of the BLASTN search enclosed herewith and the disclosure of Eikmanns et al., Applicants had possession of the claimed subject at the time the present application was filed. Accordingly, the written description requirement is satisfied, and withdrawal of this ground of rejection is respectfully requested.

Application No. 09/419,611
Reply to Office Action of August 25, 2004

The rejection under 35 U.S.C. §112, second paragraph, is respectfully traversed.

Claim 11 has been amended to specify that the citrate synthase gene is obtainable by PCR amplification of chromosomal DNA using primers of SEQ ID NO: 1 and SEQ ID NO:

2. Claims 15 and 17 have been cancelled.

In view of the foregoing, the claims are definite within the meaning of 35 U.S.C. §112, second paragraph. Accordingly, withdrawal of this ground of rejection is respectfully requested.

Applicants submit that the present application is in condition for allowance. Early notice to this effect is earnestly solicited.

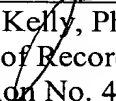
Respectfully submitted,

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Norman F. Oblon

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(OSMMN 06/04)



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Attorney of Record
Registration No. 41,504

BLASTN Search Result

Computed at GenomeNet BLAST2 Server (Kyoto Center) on Thu Jan 6 11:07:20 JST 2005

Database Name NR-NT

>query

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WARNING: possibly wrong combination

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database: nr-nt (nucl)

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blastp	prot	prot
blastn	nucl	nucl
blastx	nucl	prot
tblastn	prot	nucl
tblastx	nucl	nucl

BLASTN 2.2.10 [Oct-19-2004]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= query

(1314 letters)

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05-01-04

46,340,936 sequences; 80,264,366,952 total letters

Searching.....done

Sequences producing significant alignments:

	Score (bits)	E Value
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Top 10

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
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Length = 3013



Score = 2557 bits (1290), Expect = 0.0
Identities = 1308/1314 (99%)
Strand = Plus / Plus

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Query: 61 ggcgagttcgaatggacatcatcgaggcttctgagggtacaacggtgttgctcctgggc 120
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Query: 121 aagatgctgtctgagactggactgatcacttttgaccaggttatgtgagcactggctcc 180
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Query: 181 accgagtcgaagatcacctacatcgatggcgatgcggaatcctgcgttaccgaggctat 240
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4-5, complete genome; segment 3/10
Length = 348475

Score = 2557 bits (1290), Expect = 0.0
Identities = 1308/1314 (99%)
Strand = Plus / Plus

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Identities = 1308/1314 (99%)
Strand = Plus / Plus

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Score = 2551 bits (1287), Expect = 0.0
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Strand = Plus / Plus

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[Top](#)

Score = 2551 bits (1287), Expect = 0.0
Identities = 1305/1311 (99%)
Strand = Plus / Plus

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|||||
Sbjct: 541 gctgctagcacaccgcgacgcaagggtgctccttacatgtaccagacaactccctc 600

Query: 601 aacgcgctgagaacttcctgcgcatgatgttcggttacccaaccgagccatacagatc 660
|| |||||
Sbjct: 601 aatgcgctgagaacttcctgcgcatgatgttcggttacccaaccgagccatacagatc 660

Query: 661 gacccaatcatggtcaaggctctggacaagctgctcatcctgcacgctgaccacgagcag 720
|||||
Sbjct: 661 gacccaatcatggtcaaggctctggacaagctgctcatcctgcacgctgaccacgagcag 720

Query: 721 aactgctccacctccaccgttcgtatgatcggttcgcacaggccaacatgtttgtctcc 780
|||||
Sbjct: 721 aactgctccacctccaccgttcgtatgatcggttcgcacaggccaacatgtttgtctcc 780

Query: 781 atcgctggtggcatcaacgctctgtccggccactgcacggtggcgcaaaccaggctgtt 840
|||||
Sbjct: 781 atcgctggtggcatcaacgctctgtccggccactgcacggtggcgcaaaccaggctgtt 840

Query: 841 ctggagatgctcgaagacatcaagaacaaccacggtggcgacgcaaccgctcatgaac 900
|||||
Sbjct: 841 ctggagatgctcgaagacatcaagagcaaccacggtggcgacgcaaccgagttcatgaac 900

Query: 901 aaggtaagaacaaggaagacggcgctccgcctcatgggcttcggacaccgctttacaag 960
|||||
Sbjct: 901 aaggtaagaacaaggaagacggcgctccgcctcatgggcttcggacaccgctttacaag 960

Query: 961 aactacgatccacgtgcagcaatcgtcaaggagaccgcacacgagatcctcgagcacctc 1020
|||||
Sbjct: 961 aactacgatccacgtgcagcaatcgtcaaggagaccgcacacgagatcctcgagcacctc 1020


Query: 1021 ggtggcgacgatcttcttgatctggcaatcaagctggaagaaattgcactggctgatgat 1080
|||||
Sbjct: 1021 ggtggcgacgatcttcttgatctggcaatcaagctggaagaaattgcactggctgatgat 1080

Query: 1081 tacttcatctcccgcaagctctaccggaacgtagacttctacaccggcctgatctaccgc 1140
|||||
Sbjct: 1081 tacttcatctcccgcaagctctaccggaacgtagacttctacaccggcctgatctaccgc 1140

Query: 1141 gcaatgggcttcccaactgacttcttcaccgtattgttcgcaatcggtcgtctgccagga 1200
|||||
Sbjct: 1141 gcaatgggcttcccaactgacttcttcaccgtattgttcgcaatcggtcgtctgccagga 1200

Query: 1201 tggatcgctcactaccgagcagctcggtgcagcaggcaacaagatcaaccgcccacgc 1260
|||||
Sbjct: 1201 tggatcgctcactaccgagcagctcggtgcagcaggcaacaagatcaaccgcccacgc 1260

Query: 1261 caggctctacaccggaaggaatcccgcaagttggttcctcgcgaggagcgc 1311
|||||
Sbjct: 1261 caggctctacaccggaacgaatcccgcaagttggttcctcgcgaggagcgc 1311

>gb:AP005217 [AP005217] *Corynebacterium efficiens* YS-314 DNA, complete genome,  [Top](#)
section 4/11.
Length = 300750

Score = 1110 bits (560), Expect = 0.0
Identities = 1096/1273 (86%), Gaps = 5/1273 (0%)
Strand = Plus / Plus

Query: 3 gtttgaaaggatctgtggctactgataacaacaaggctgtcctgcactaccccggtgg 62
|||||
Sbjct: 22750 gtttgaaaggaaatcgtggcttctgataacaacaaggctgtactgcactaccctggcgg 22809

Query: 63 cgagttcgaaatggacatcatcgaggcttctgagggttaacaacggtgttgcctgggcaa 122
||| |||||
Sbjct: 22810 cgaattcgagatgggcatcaagcaggccaccgagggttaactccggtgtcatcctgggtaa 22869

Query: 123 gatgctgtctgagactggactgatcacttttgaccaggttatgtgagcactggctccac 182
|||||
Sbjct: 22870 gatgctgtcggaaaccggtctggtcaccttcgaccccggttatgtcagcaccggttccac 22929

Query: 183 cgagtcgaagatcacctacatcgatggcgatgcgggaatcctgcgttaccgcggtatga 242
||| |||
Sbjct: 22930 cgaatccaagatcacctacatcgatggtgatgcaggcatcctgcgctaccgcggtacga 22989

Query: 243 catcgctgatctggctgagaatgccaccttcaacgaggtttcttacctattatcaacgg 302
||| |||
Sbjct: 22990 cattcggtatctggccgaaaatgccaccttcaatgaggtctcctacctcctgatcaaggg 23049

Query: 303 tgaactaccaaccccagatgagcttcacaagtttaacgacgagattcgccaccacaccct 362
||| |||
Sbjct: 23050 tgagctcccgaccccggaagagctccacaagtttaacgacgagattcgtcaccacaccct 23109

Query: 363 tctggacgaggacttcaagtccagttcaactgttccacgcgacgctcacccaatggc 422
|||||
Sbjct: 23110 gctggacgaggacttcaagtccagttcaatgtcttccctcgcgatgccacccgatggc 23169

Query: 423 aaccttggttctcctcggttaacattttgtctacctactaccaggatcagctgaaccact 482
||| |||
Sbjct: 23170 caccctggcctcctcggttaacatcctctccacctactaccaggatcagctggatcccct 23229

Query: 483 cgatgaggcacagcttgataaggcaaccgttcgcctcatggcaaaggttccaatgctggc 542
|||||
Sbjct: 23230 ggatgaggctcagctggacaaggcaaccgttcgcctcatggcaaaggttccgatgctggc 23289

Query: 543 tgcgtacgcacaccgcgcacgcaagggtgtccttacatgtacccagacaactccctcaa 602
||| |||
Sbjct: 23290 tgcatacgcacaccgtgcccgaagggtgcgcctacatgtacccggacaactccctcaa 23349

Query: 603 cgcgctgagaacttctcgtcgtatgatgttcggttacccaaccgagccatacagatcga 662
||| |||

file:///C:/¥Documents%20and%20Settings¥kagaku7¥Local%20Settings¥Temporary%2... 2005/01/06

Posted date: Jan 4, 2005 6:06 AM
Number of letters in database: 1,999,861,861
Number of sequences in database: 370,666

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.02
Posted date: Jan 4, 2005 6:13 AM
Number of letters in database: 1,999,963,845
Number of sequences in database: 360,118

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.03
Posted date: Jan 4, 2005 6:28 AM
Number of letters in database: 1,999,999,976
Number of sequences in database: 3,329,958

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.04
Posted date: Jan 4, 2005 6:45 AM
Number of letters in database: 1,999,999,708
Number of sequences in database: 3,404,633

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.05
Posted date: Jan 4, 2005 7:03 AM
Number of letters in database: 1,999,999,998
Number of sequences in database: 3,904,937

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.06
Posted date: Jan 4, 2005 7:23 AM
Number of letters in database: 1,999,999,553
Number of sequences in database: 4,328,864

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.07
Posted date: Jan 4, 2005 7:42 AM
Number of letters in database: 1,999,999,957
Number of sequences in database: 3,891,732

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.08
Posted date: Jan 4, 2005 7:59 AM
Number of letters in database: 1,999,999,671
Number of sequences in database: 3,486,474

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.09
Posted date: Jan 4, 2005 8:23 AM
Number of letters in database: 1,999,999,859
Number of sequences in database: 3,293,154

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.10
Posted date: Jan 4, 2005 8:41 AM
Number of letters in database: 1,999,999,669
Number of sequences in database: 3,828,471

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.11
Posted date: Jan 4, 2005 8:57 AM
Number of letters in database: 1,999,999,424
Number of sequences in database: 2,772,633

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.12
Posted date: Jan 4, 2005 9:05 AM
Number of letters in database: 1,999,921,952
Number of sequences in database: 631,119

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.13
Posted date: Jan 4, 2005 9:13 AM
Number of letters in database: 1,999,956,728
Number of sequences in database: 16,152

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.14

Posted date: Jan 4, 2005 9:19 AM
Number of letters in database: 1,999,893,819
Number of sequences in database: 9139

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.15
Posted date: Jan 4, 2005 9:25 AM
Number of letters in database: 1,999,809,626
Number of sequences in database: 8148

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.16
Posted date: Jan 4, 2005 9:32 AM
Number of letters in database: 1,999,958,517
Number of sequences in database: 9281

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.17
Posted date: Jan 4, 2005 9:39 AM
Number of letters in database: 1,999,869,985
Number of sequences in database: 118,685

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.18
Posted date: Jan 4, 2005 9:46 AM
Number of letters in database: 1,999,869,072
Number of sequences in database: 575,666

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.19
Posted date: Jan 4, 2005 9:55 AM
Number of letters in database: 1,999,866,894
Number of sequences in database: 705,081

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.20
Posted date: Jan 4, 2005 10:02 AM
Number of letters in database: 1,999,925,325
Number of sequences in database: 63,082

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.21
Posted date: Jan 4, 2005 10:10 AM
Number of letters in database: 1,999,999,826
Number of sequences in database: 569,309

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.22
Posted date: Jan 4, 2005 10:22 AM
Number of letters in database: 1,997,416,774
Number of sequences in database: 2,119,519

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.23
Posted date: Jan 4, 2005 10:29 AM
Number of letters in database: 1,999,944,509
Number of sequences in database: 107,016

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.24
Posted date: Jan 4, 2005 10:36 AM
Number of letters in database: 1,999,998,745
Number of sequences in database: 293,074

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.25
Posted date: Jan 4, 2005 10:45 AM
Number of letters in database: 1,999,996,900
Number of sequences in database: 1,064,738

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.26
Posted date: Jan 4, 2005 10:55 AM
Number of letters in database: 1,999,992,337
Number of sequences in database: 933,438

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.27

Posted date: Jan 4, 2005 11:02 AM
Number of letters in database: 1,999,979,685
Number of sequences in database: 288,812

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.28
Posted date: Jan 4, 2005 11:09 AM
Number of letters in database: 1,999,992,360
Number of sequences in database: 288,789

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.29
Posted date: Jan 4, 2005 11:16 AM
Number of letters in database: 1,999,991,524
Number of sequences in database: 89,111

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.30
Posted date: Jan 4, 2005 11:23 AM
Number of letters in database: 1,999,976,519
Number of sequences in database: 217,802

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.31
Posted date: Jan 4, 2005 11:29 AM
Number of letters in database: 1,999,995,610
Number of sequences in database: 136,831

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.32
Posted date: Jan 4, 2005 11:36 AM
Number of letters in database: 1,999,921,996
Number of sequences in database: 162,607

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.33
Posted date: Jan 4, 2005 11:43 AM
Number of letters in database: 1,999,964,690
Number of sequences in database: 218,162

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.34
Posted date: Jan 4, 2005 11:50 AM
Number of letters in database: 1,999,976,965
Number of sequences in database: 61,666

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.35
Posted date: Jan 4, 2005 11:57 AM
Number of letters in database: 1,999,991,196
Number of sequences in database: 368,188

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.36
Posted date: Jan 4, 2005 12:05 PM
Number of letters in database: 1,999,904,998
Number of sequences in database: 477,581

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.37
Posted date: Jan 4, 2005 12:11 PM
Number of letters in database: 1,999,925,109
Number of sequences in database: 63,652

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.38
Posted date: Jan 4, 2005 12:18 PM
Number of letters in database: 1,999,998,888
Number of sequences in database: 310,761

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.39
Posted date: Jan 4, 2005 12:25 PM
Number of letters in database: 1,998,257,110
Number of sequences in database: 177,152

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.40

Posted date: Jan 4, 2005 12:26 PM
Number of letters in database: 270,246,158
Number of sequences in database: 39,235

Lambda	K	H
1.37	0.711	1.31

Gapped

Lambda	K	H
1.37	0.711	1.31

Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 36,390,912
Number of Sequences: 46340936
Number of extensions: 36390912
Number of successful extensions: 627339
Number of sequences better than 10.0: 220
Number of HSP's better than 10.0 without gapping: 220
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 624290
Number of HSP's gapped (non-prelim): 3035
length of query: 1314
length of database: 80,264,366,952
effective HSP length: 24
effective length of query: 1290
effective length of database: 79,152,184,488
effective search space: 102106317989520
effective search space used: 102106317989520
T: 0
A: 0
X1: 11 (21.8 bits)
X2: 15 (29.7 bits)
S1: 12 (24.3 bits)
S2: 22 (44.1 bits)

=

BLASTP Search Result

Computed at GenomeNet BLAST2 Server (Kyoto Center) on Thu Jan 6 11:02:36 JST 2005

Database Name NR-AA

>query

```

MFERDIVATD NNAVLHYPG GEFEMDIEA SEGNGVVLG KMLSETGLIT
FDPGYVSTGS TESKITYIDG DAGILRYRGY DIADLAENAT FNEVSYLLIN
GELPTDELH KFNDEIRHHT LLEDFKSQF NVFPRDAHPM ATASSVNIL
STYYQDQLNP LDEAQLDKAT VRLMAKVPML AAYAHRARKG APYMPDNSL
NARENFLRMM FGYPTEPYEI DPIMVKALDK LLILHADHEQ NCSTSTVRMI
GSAQANMFVS IAGGINALSG PLHGGANQAV LEMLEDIKNN HGGDATAFMN
KVKNKEDGVR LMGFGHRVYK NYDPRAAIVK ETAHEILEHL GGDDLLDLAI
KLEEIALADD YFISRKLYPN VDFYTGLIYR AMGFPTDFFT VLFAIGRLPG
WIAHYREQLG AAGNKINRPR QVYTGKESRK LVPREER*

```

BLASTP 2.2.10 [Oct-19-2004]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= query
(437 letters)

Database: nr-aa: Non-redundant protein sequence database Release
05-01-04

1,848,798 sequences; 600,567,511 total letters

Searching.....done

Sequences producing significant alignments:

	Score (bits)	E Value
--	-----------------	------------

Top 10	<input type="checkbox"/>	Clear	Select operation	<input type="checkbox"/>	Exec
<input checked="" type="checkbox"/>	sp:CISY_CORGL	[P42457]	Citrate synthase (EC 2.3.3.1).	>pir:I40717...	855 0.0
<input checked="" type="checkbox"/>	gp:AX065419_1	[AX065419]	Sequence 545 from Patent W00100844.	[Co...	842 0.0
<input checked="" type="checkbox"/>	tr:Q8RQP3	[Q8RQP3]	Citrate synthase (EC 2.3.3.1).	>gpu:BA000035_9...	798 0.0
<input checked="" type="checkbox"/>	tr:Q6NIJ0	[Q6NIJ0]	Citrate synthase (EC 2.3.3.1).	>trnew:CAE49303...	750 0.0
<input checked="" type="checkbox"/>	tr:Q9RMRO	[Q9RMRO]	Citrate synthase.	>gp:AF191033_1 [AF191033] ci...	548 e-155
<input checked="" type="checkbox"/>	tr:Q5Z238	[Q5Z238]	Putative citrate synthase.	>gpu:AP006618_661 [...]	546 e-154
<input checked="" type="checkbox"/>	tr:Q9R339	[Q9R339]	Citrate synthase (EC 4.1.3.7).	>gpu:SC0939113_...	536 e-151
<input checked="" type="checkbox"/>	tr:Q7U122	[Q7U122]	PROBABLE CITRATE SYNTHASE I GLTA2 (EC 2.3.3.1...		535 e-150
<input checked="" type="checkbox"/>	sp:CISY_MYCTU	[Q10530]	Citrate synthase 1 (EC 2.3.3.1).	>pir:E707...	535 e-150
<input checked="" type="checkbox"/>	tr:Q82CL5	[Q82CL5]	Putative citrate synthase.	>gpu:BA000030_5334 ...	533 e-150

>sp:CISY_CORGL [P42457] Citrate synthase (EC 2.3.3.1).>pir:I40717 [I40717] citrate ▲Top
(si)-synthase (EC 4.1.3.7) - Corynebacterium
glutamicum>prf:2106273A citrate synthase -
Corynebacterium glutamicum>gpu:BA000036_829 [BA000036]
Citrate synthase [Corynebacterium glutamicum ATCC 13032]
Length = 437

Score = 855 bits (2209), Expect = 0.0
Identities = 425/437 (97%), Positives = 426/437 (97%)

Query: 1 MFERDIVATDNNKAVLHYPGGEFEMDI IEASEGNNGVVLGKMLSETGLITFDPGYVSTGS 60
MFERDIVATDNNKAVLHYPGGEFEMDI IEASEGNNGVVLGKMLSETGLITFDPGYVSTGS
Sbjct: 1 MFERDIVATDNNKAVLHYPGGEFEMDI IEASEGNNGVVLGKMLSETGLITFDPGYVSTGS 60

Query: 61 TESKITYIDGDAGILRYRGYDIADLAENATFNEVSYLLINGELPTDELHKFNDEIRHHT 120
TESKITYIDGDAGILRYRGYDIADLAENATFNEVSYLLINGELPTDELHKFNDEIRHHT
Sbjct: 61 TESKITYIDGDAGILRYRGYDIADLAENATFNEVSYLLINGELPTDELHKFNDEIRHHT 120

Query: 121 LLEDEFKSQFNVFPRDAHPMATLASSVNI LSTYYQDQLNPLDEAQLDKATVRLMAKVPML 180
LLEDEFKSQFNVFPRDAHPMATLASSVNI LSTYYQDQLNPLDEAQLDKATVRLMAKVPML
Sbjct: 121 LLEDEFKSQFNVFPRDAHPMATLASSVNI LSTYYQDQLNPLDEAQLDKATVRLMAKVPML 180


Query: 181 AAYAHRARKGAPYMPDNSLNARENFLRMMFGYPTEPYEIDPIMVKALDKLLILHADHEQ 240
AAYAHRARKGAPYMPDNSLNARENFLRMMFGYPTEPYEIDPIMVKALDKLLILHADHEQ
Sbjct: 181 AAYAHRARKGAPYMPDNSLNARENFLRMMFGYPTEPYEIDPIMVKALDKLLILHADHEQ 240

Query: 241 NCSTSTVRMIGSAQANMFVSIAGGINALSGPLHGGANQAVLEMLEDIKNNHGGDATAFMN 300
NCSTSTVRMIGSAQANMFVSIAGGINALSGPLHGGANQAVLEMLEDIK+NHGGDAT FMN
Sbjct: 241 NCSTSTVRMIGSAQANMFVSIAGGINALSGPLHGGANQAVLEMLEDIKSNHGGDATEFMN 300

Query: 301 KVKNKEDGVRLMGFGHRVYKNDPRAAIVKETAHEILEHXXXXXXXXXAIKLEEIALADD 360
KVKNKEDGVRLMGFGHRVYKNDPRAAIVKETAHEILEH AIKLEEIALADD
Sbjct: 301 KVKNKEDGVRLMGFGHRVYKNDPRAAIVKETAHEILEHGGDDLDDLAIKLEEIALADD 360

Query: 361 YFISRKLYPNVDFYTGLIYRAMGFPTDFFTVLFAIGRLPGWIAHYREQLGAAGNKINRPR 420
YFISRKLYPNVDFYTGLIYRAMGFPTDFFTVLFAIGRLPGWIAHYREQLGAAGNKINRPR
Sbjct: 361 YFISRKLYPNVDFYTGLIYRAMGFPTDFFTVLFAIGRLPGWIAHYREQLGAAGNKINRPR 420

Query: 421 QVYTGKESRKLVPREER 437
QVYTG ESRKLVPREER
Sbjct: 421 QVYTGNESRKLVPREER 437

>gp:AX065419_1 [AX065419] Sequence 545 from Patent W00100844. [Corynebacterium  Top
glutamicum]
Length = 431

Score = 842 bits (2175), Expect = 0.0
Identities = 418/431 (96%), Positives = 420/431 (97%)

Query: 7 VATDNNKAVLHYPGGEFEMDI IEASEGNNGVVLGKMLSETGLITFDPGYVSTGSTESKIT 66
+ATDNNKAVLHYPGGEFEMDI IEASEGNNGVVLGKMLSETGLITFDPGYVSTGSTESKIT
Sbjct: 1 MATDNNKAVLHYPGGEFEMDI IEASEGNNGVVLGKMLSETGLITFDPGYVSTGSTESKIT 60

Query: 67 YIDGDAGILRYRGYDIADLAENATFNEVSYLLINGELPTDELHKFNDEIRHHTLLEDEF 126
YIDGDAGILRYRGYDIADLAENATFNEVSYLLINGELPTDELHKFNDEIRHHTLLEDEF
Sbjct: 61 YIDGDAGILRYRGYDIADLAENATFNEVSYLLINGELPTDELHKFNDEIRHHTLLEDEF 120

Query: 127 KSQFNVFPRDAHPMATLASSVNI LSTYYQDQLNPLDEAQLDKATVRLMAKVPMLAAYAHR 186
KSQFNVFPRDAHPMATLASSVNI LSTYYQDQLNPLDEAQLDKATVRLMAKVPMLAAYAHR
Sbjct: 121 KSQFNVFPRDAHPMATLASSVNI LSTYYQDQLNPLDEAQLDKATVRLMAKVPMLAAYAHR 180

Query: 187 ARKGAPYMPDNSLNARENFLRMMFGYPTEPYEIDPIMVKALDKLLILHADHEQNCSTST 246
ARKGAPYMPDNSLNARENFLRMMFGYPTEPYEIDPIMVKALDKLLILHADHEQNCSTST
Sbjct: 181 ARKGAPYMPDNSLNARENFLRMMFGYPTEPYEIDPIMVKALDKLLILHADHEQNCSTST 240

Query: 247 VRMIGSAQANMFVSIAGGINALSGPLHGGANQAVLEMLEDIKNNHGGDATAFMNKVKNKE 306
VRMIGSAQANMFVSIAGGINALSGPLHGGANQAVLEMLEDIK+NHGGDAT FMNKVKNKE
Sbjct: 241 VRMIGSAQANMFVSIAGGINALSGPLHGGANQAVLEMLEDIKSNHGGDATEFMNKVKNKE 300

Query: 307 DGVRLMGFGHRVYKNDPRAAIVKETAHEILEHXXXXXXXXXAIKLEEIALADDYFISRK 366
DGVRLMGFGHRVYKNDPRAAIVKETAHEILEH AIKLEEIALADDYFISRK
Sbjct: 301 DGVRLMGFGHRVYKNDPRAAIVKETAHEILEHGGDDLDDLAIKLEEIALADDYFISRK 360

Query: 367 LYPNVDFYTGLIYRAMGFPTDFFTFLFAIGRLPGWIAHYREQLGAAGNKINRPRQVYTGK 426
LYPNVDFYTGLIYRAMGFPTDFFTFLFAIGRLPGWIAHYREQLGAAGNKINRPRQVYTG
Sbjct: 361 LYPNVDFYTGLIYRAMGFPTDFFTFLFAIGRLPGWIAHYREQLGAAGNKINRPRQVYTGN 420

Query: 427 ESRKLVPREER 437
ESRKLVPREER
Sbjct: 421 ESRKLVPREER 431

>tr:Q8RQP3 [Q8RQP3] Citrate synthase (EC 2.3.3.1).>gpu:BA000035_903 [BA000035] [▲Top](#)
citrate synthase [Corynebacterium efficiens
YS-314]>gp:AB082520_1 [AB082520] citrate synthase
[Corynebacterium efficiens]>gp:AP005217_19 [AP005217]
citrate synthase [Corynebacterium efficiens YS-314]
Length = 470

Score = 798 bits (2060), Expect = 0.0
Identities = 394/436 (90%), Positives = 413/436 (94%), Gaps = 1/436 (0%)

Query: 2 FERDIVATDNNKAVLHYPGGEFEMDIEASEGNNGVVLGKMLSETGLITFDPGYVSTGST 61
FER+IVA+DNNKAVLHYPGGEFEM I +A+EGN+GV+LGKMLSETGL+TFDPGYVSTGST
Sbjct: 36 FERIVASDNNKAVLHYPGGEFEMGIKQATEGNSGVILGKMLSETGLVTFDPGYVSTGST 95

Query: 62 ESKITYIDGDAGILRYRGYDIADLAENATFNEVSYLLINGELPTDELHKFNDEIRHHTL 121
ESKITYIDGDAGILRYRGYDIADLAENATFNEVSYLLI GELPTP+ELHKFNDEIRHHTL
Sbjct: 96 ESKITYIDGDAGILRYRGYDIADLAENATFNEVSYLLIKGELPTPEELHKFNDEIRHHTL 155

Query: 122 LDEDFKSQFNVFPRDAHMPATLASSVNI LSTYYQDQLNPLDEAQLDKATVRLMAKVPMLA 181
LDEDFKSQFNVFPRDAHMPATLASSVNI LSTYYQDQL+PLDEAQLDKATVRLMAKVPMLA
Sbjct: 156 LDEDFKSQFNVFPRDAHMPATLASSVNI LSTYYQDQLDPLDEAQLDKATVRLMAKVPMLA 215

Query: 182 AYAHRRARKGAPYMPDNSLNARENFLRMMFGYPTEPYEIDPIMVKALDKLLILHADHEQN 241
AYAHRRARKGAPYMPDNSLNARENFLRMMFGYPTEPYE+DPIMVKALDKLLILHADHEQN
Sbjct: 216 AYAHRRARKGAPYMPDNSLNARENFLRMMFGYPTEPYEVDPI MVKALDKLLILHADHEQN 275

Query: 242 CSTSTVRMIGSAQANMFVSIAGGINALSGPLHGGANQAVLEMLEDIKNNHGGDATAFMNK 301
CSTSTVRMIGSAQANMFVSIAGGINALSGPLHGGANQAVLEMLE+I N GGDAT FMN+
Sbjct: 276 CSTSTVRMIGSAQANMFVSIAGGINALSGPLHGGANQAVLEMLEEIAAN-GGDATDFMNR 334

Query: 302 VKNKEDGVRLMGFGRVYKNDPRAAIVKETAHEILEHXXXXXXXXXA KLEEIALADDY 361
VKNKE GVRMLMGFGRVYKNDPRAAIVK+TAHEILEH A+KLEEIAL DDY
Sbjct: 335 VKNKEGVRLMGFGRVYKNDPRAAIVKDTAHEILEHLGGDPLLDLALKLEEIALNDDY 394

Query: 362 FISRKLYPNVDFYTGLIYRAMGFPTDFFTFLFAIGRLPGWIAHYREQLGAAGNKINRPRQ 421
FISRKLYPNVDFYTGLIYRAMGFPTDFFTFLFAIGRLPGWIAHYREQL G KINRPRQ
Sbjct: 395 FISRKLYPNVDFYTGLIYRAMGFPTDFFTFLFAIGRLPGWIAHYREQLADPGAKINRPRQ 454

Query: 422 VYTGKESRKLVPREER 437
+YTG+ +RK++PREER
Sbjct: 455 IYTGETARKIIPREER 470

>tr:Q6NIJ0 [Q6NIJ0] Citrate synthase (EC 2.3.3.1).>trnew:CAE49303 [CAE49303] [▲Top](#)
Citrate synthase (EC 2.3.3.1).>gpu:BX248356_61
[BX248356] citrate synthase [Corynebacterium
diphtheriae]>gp:BX248356_61 [BX248356] citrate synthase
[Corynebacterium diphtheriae]
Length = 435

Score = 750 bits (1937), Expect = 0.0
Identities = 371/433 (85%), Positives = 401/433 (92%), Gaps = 3/433 (0%)

Query: 6 IVATDN-NKAVLHYPGGEFEMDIEASEGNNGVVLGKMLSETGLITFDPGYVSTGSTESK 64

+VAT+N +KAVLHYPGGE+EMDII A+EGN+GVVL K+LS+TG++TFDPGYVSTGSTESK
Sbjct: 5 LVATENKDKAVLHYPGGEYEMDIIHATEGNDGVVLKLLSQTGMVTFDPGYVSTGSTESK 64

Query: 65 ITYIDGDAGILRYRGYDIADLAENATFNEVSYLLINGELPTDELHKFNDEIRHHTLLDE 124
ITYIDGD GILR+RGYDIADLAENATFNEVSYLLI G LPT DELHKFN+EIRHHTLLDE
Sbjct: 65 ITYIDGDNGILRHRGYDIADLAENATFNEVSYLLIKGHLPTVDELHKFNNEIRHHTLLDE 124

Query: 125 DFKSQFNVPFPRDAHMPATLASSVNI LSTYYQDQLNPLDEAQLDKATVRLMAKVPMLAAYA 184
DFKSQFN+FPFPRDAHMP+ LASSVNI LSTYYQDQLNPLDE QLDKATVRL+AKVPMLAAYA
Sbjct: 125 DFKSQFNI FPRDAHMPMSVLASSVNI LSTYYQDQLNPLDEEQDKATVRLAKVPMLAAYA 184

Query: 185 HRARKGAPYMPDNSLNARENFLRMMFGYPTEPYEIDPIMVKALDKLLILHADHEQNCST 244
+RA KGAPYMPDNSLNARENFLRMMFGYPTEPYE+DP++ KALDKLLILHADHEQNCST
Sbjct: 185 YRASKGAPYMPDNSLNARENFLRMMFGYPTEPYEVDPPVAKALDKLLILHADHEQNCST 244

Query: 245 STVRMIGSAQANMFVSIAGGINALSGPLHGGANQAVLEMLEDIKNNHGGDATAFMNKVKN 304
STVRMIGSAQANMFV++AGGINALSGPLHGGANQAVLEMLE+IK N GGDAT FMN+VKN
Sbjct: 245 STVRMIGSAQANMFVAVAGGINALSGPLHGGANQAVLEMLEEIKAN-GGDATDFMNRVKN 303

Query: 305 KEDGVRLMGFGHRVYKNDPRAAIVKETAHEILEHXXXXXXXXXA KLEEIALADDYFIS 364
KE GVRLMGFGHRVYKNDPRAAIVKETAHEILEH A+KLEEIAL+DDYF+S
Sbjct: 304 KEGVRLMGFGHRVYKNDPRAAIVKETAHEILEHLGGDELLDLAMKLEEIALSDDYFVS 363

Query: 365 RKLYPNVDFYTGLIYRAMGFPTDFFTVLFAIGRLPGWIAHYREQLGAAGNKINRPRQVYT 424
RKLYPNVDFYTGLIYRAMGFPTDFFTVLFAIGRLPGWIA YREQL A KINRPRQ+YT
Sbjct: 364 RKLYPNVDFYTGLIYRAMGFPTDFFTVLFAIGRLPGWIAQYREQL-ATTTKINRPRQIYT 422

Query: 425 GKESRKLVPREER 437
G+ RK+ PRE+R
Sbjct: 423 GETLRKVTPREQR 435

>tr:Q9RMR0 [Q9RMR0] Citrate synthase.>gp:AF191033_1 [AF191033] citrate
synthase [Mycobacterium smegmatis]
Length = 441

▲Top

Score = 548 bits (1413), Expect = e-155

Identities = 272/421 (64%), Positives = 328/421 (77%), Gaps = 2/421 (0%)

Query: 18 YPGGEFEMDII EASEGNNGVVLGKMLSETGLITFDPGYVSTGSTESKITYIDGDAGILRY 77
YPGG+ E+ I++A+EG + V LGK L+ET L TFD G+++T ST+S ITYIDG+ GILRY
Sbjct: 22 YPGGKLELPILKATEGTDSVALGKFLAETNLTFDSGFMNTASTKSAITYIDGEQGILRY 81

Query: 78 RGYDIADLAENATFNEVSYLLINGELPTDELHKFNDEIRHHTLLDEDFKSQFNVPFPRDA 137
RG I LAE +TF EVSYLLI GELPTP +L +F +I+ HTLL ED K F+ FPR+A
Sbjct: 82 RGIPIEQLAEKSTFIEVSYLLIYGELPTPTQLEEF TTKIQRHTLLHEDLKRFFDGFPRNA 141

Query: 138 HPMATLASSVNI LSTYYQDQLNPLDEAQLDKATVRLMAKVPMLAAYHRARKGAPYMPD 197
HPM L+S+VN LS YYQD L+P D+ Q++ +T+RL+AK+P +AAYA++ G P++YPD
Sbjct: 142 HPMPVLSSAVNALSAYYQDSLDPKDDEQVELSTIRLLAKLPTIAAYAYKKSAGQPFYPD 201

Query: 198 NSLNARENFLRMMFGYPTEPYEIDPIMVKALDKLLILHADHEQNCSTSTVRMIGSAQANM 257
NSL+ ENFLRM FG+P EPYE++P + KALD L ILHADHEQNCSTSTVR++GS+QAN+
Sbjct: 202 NSLSLVENFLRMTFGFPAEPYEVNPDVAKALDMLF ILHADHEQNCSTSTVRLVGSSQANL 261

Query: 258 FVSIAGGINALSGPLHGGANQAVLEMLEDIKNNHGGDATAFMNKVKNKEDGVRLMGFGHR 317
F SI+GGINAL GPLHGGANQAVLEML+ IK + GGD FM +VKNKE GV+LMGFGHR
Sbjct: 262 FTSISGINALWGPLHGGANQAVLEMLDAIKAD-GGDTKKFMERVKNKEAGVKLMGFGHR 320

Query: 318 VYKNYDPRAAIVKETAHEILEHXXXXXXXXXA K-LEEIALADDYFISRKLYPNVDFYTG 376
VYKNYDPRAAIVK+TA +ILE K LEE+AL DDYFI RKLYPNVDFYTG
Sbjct: 321 VYKNYDPRAAIVKKTADQILETLGVQDDLLEIAKGLEEVALNDDYFIERKLYPNVDFYTG 380

Query: 377 LIYRAMGFPTDFFTVLFAIGRLPGWIAHYREQLGAAGNKINRPRQVYTGKESRKLVPREE 436

+IYRAMGFPT FTVLFA+GRLPGWIAH+RE KI RPRQ+YTG R VP +
Sbjct: 381 VIYRAMGFPTRMFTVLFA+GRLPGWIAH+REMHEDPTTKIGRPRQLYTGYTERDYVPMSD 440

Query: 437 R 437

R

Sbjct: 441 R 441

>tr:Q5Z238 [Q5Z238] Putative citrate synthase. >gpu:AP006618_661 [AP006618] ▲Top
putative citrate synthase [Nocardia farcinica IFM
10152]>gp:AP006618_661 [AP006618] putative citrate
synthase [Nocardia farcinica]
Length = 433

Score = 546 bits (1406), Expect = e-154

Identities = 270/421 (64%), Positives = 328/421 (77%), Gaps = 3/421 (0%)

Query: 10 DNNKAVLHYPGGFEMDII EASEGNGVVLGKMLSETGLITFDPGYVSTGSTESKITYID 69
D+ K VL YPGGE+ M I EA+EGN+G+ LGKML+ TG +T+DPG+++T T+S ITYID
Sbjct: 7 DDAKPVLSYPGGEYAMTITEATEGNHGIDLKMLASTGYVTYDPGFMNTAPTksAITYID 66

Query: 70 GDAGILRYRGYDIADLAENATFNEVSyllINGELPTDELHKFNDEIRHHTLLDEDFKSQ 129
G+AGILRYRGY I LA+++TF EVSYLLI GELPT +L F D IR HTLL ED K
Sbjct: 67 GEAGILRYRGYPIEQLADSSTFIEVSyllIYGELPTQAQLDDFTDIRRHHTLLHEDLKRF 126

Query: 130 FNVFPRDAHPMATLASSVNI LSTYYQDQLNPLDEAQLDKATVRLMAKVPM LAAYHRARK 189
F+ FPR+AHPM L+S+VN LS YYQD L+P D Q++ +T+RL+AK+P +AAY+++
Sbjct: 127 FDGFPRNAHPMPVLSSAVNALSAYYQDSLDPDPEQVELSTIRLLAKLPTIAAYS YKKS V 186

Query: 190 GAPYMPDNLNARENFLRMMFGYPTPEYIDPIMVKALDKLLILHADHEQNCSTSTVRM 249
G P++YPDNL ENFLRM FG+P EPYE+DP + ALD LLILHADHEQNCSTSTVR+
Sbjct: 187 GQPFLYPDNLTLVENFLRMTFGFAEPYEVDP EVAALDMLLILHADHEQNCSTSTVRL 246

Query: 250 IGSAQANMFVSIAGGINALSGPLHGGANQAVLEMLEDIKNNHGGDATAFMNKVKNKEDGV 309
+GS+ AN+F S++GGINAL GPLHGGANQAVLEML+DIK GGD F+ KVKNKEDGV
Sbjct: 247 VGSSDANLFTSVSGGINALWGPLHGGANQAVLEMLDDIK-AQGGDVKEFIRKVKNKEDGV 305

Query: 310 RLMGFGRHRYVKNYDPRAAI VKETAHEILEH-XXXXXXXXXA I KLEEIALADDYFISRKLY 368
+LMGFGRHRYV+NYDPRAAI K+ A IL A LEE AL DDYF+ R+LY
Sbjct: 306 KLMGFGRHRYVKNYDPRAAI AKKHADN I LRKLGGDELFEIAQALEEALTDYFVERRLY 365

Query: 369 PNVDFTGLIYRAMGFPTDFFTVLFAIGRLPGWIAHYREQLGAAGNKINRPROVYTGKES 428
PNVDFTYG+IY+AMGFPT FTVLFA+GRLPGWIAH+RE + + KI RPRQ+YTG +
Sbjct: 366 PNVDFTGVIYKAMGFPTRMFTVLFA+GRLPGWIAH+RE-MHSEPLKIGRPRQIYTG YGA 424

Query: 429 R 429

R

Sbjct: 425 R 425

>tr:Q9R339 [Q9R339] Citrate synthase (EC 4.1.3.7). >gpu:SC0939113_211 ▲Top
[AL939113] citrate synthase. [Streptomyces coelicolor
A3(2)]>gp:SC0939113_211 [AL939113] citrate synthase.
[Streptomyces coelicolor A3(2)]>gp:AF181118_1 [AF181118]
citrate synthase [Streptomyces coelicolor]
Length = 429

Score = 536 bits (1382), Expect = e-151

Identities = 265/428 (61%), Positives = 327/428 (76%), Gaps = 2/428 (0%)

Query: 11 NNKAVLHYPGGFEMDII EASEGNGVVLGKMLSETGLITFDPGYVSTGSTESKITYIDG 70
+N VL Y GE+ +I+++ G+ G +GK+ ++TGL+T D GY +T + +S ITY+DG
Sbjct: 3 DNSVVLRYGDGEYTPVIDSTVGDKGFDIGKLRAQTGLVTLDSGYGNTAAYKSAITYLDG 62

Query: 71 DAGILRYRGYDIADLAENATFNEVSYLLINGELPTDELHKFNDEIRHHTLLDEDFKSQF 130
+AGILRYRGY I LAE ++F EV+YLLINGELPT DEL F EI HTLL ED K+ +
Sbjct: 63 EAGILRYRGYIEQLAERSSFEVAYLLINGELPTVDELSAFKGEITQHTLLHEDVKNFY 122

Query: 131 NVFPRDAHPMATLASSVNI LSTYYQDQLNPLDEAQLDKATVRLMAKVPMLAAYHRARKG 190
FPRDAHPMA L+S V+ LST+YQD NP DE Q + +T+RL+AK+P +AAYA++ G
Sbjct: 123 KGFPRAHPMAMLSVVSALSTFYQDSHNPFDERQRLSTIRLLAKLPTIAAYAYKKSIG 182

Query: 191 APYMPDNLNARENFLRMMFGYPTEPYEIDPIMVKALDKLLILHADHEQNCSTSTVRMI 250
P++YP N+L ENFLRM F P + YE+DP +V ALDKLLILHADHEQNCSTSTVR++
Sbjct: 183 HPFVYPANNLGYVENFLRMTFSVPAQEYELDPTVVAALDKLLILHADHEQNCSTSTVRLV 242

Query: 251 GSAQANMFVSIAGGINALSGPLHGGANQAVLEMLEDIKNNHGGDATAFMNKVKNKEDGVR 310
GS+QANMF SI+ GINAL GPLHGGANQ+VLEMLE I+ + GGD +F+ KVKNKEDGVR
Sbjct: 243 GSSQANMFASISAGINALWGPLHGGANQSVLEMLEGIR-DAGGDVDSFIRKVKNKEDGVR 301

Query: 311 LMGFGHRVYKKNYDPRAAIVKETAHEILEH-XXXXXXXXXA|KLEEIALADDYFISRKLYP 369
LMGFGHRVYKN+DPRA I+K AH++L A+KLEE AL+DDYF+SR LYP
Sbjct: 302 LMGFGHRVYKNFDPRAKIIKAAHDVLSALGKSELDLIALKLEEHALSDDYFVSRSLYP 361

Query: 370 NVDFYTGLIYRAMGFPTDFFTVLFAIGRLPGWIAHYREQLGAAGNKINRPRQVYTGKESR 429
NVDFYTGLIYRAMGFPT+ FTVLFA+GRLPGWIA + E + G++I RPRQ+YTG R
Sbjct: 362 NVDFYTGLIYRAMGFPTMFVLFALGRLPGWIAQWHEMIKEPGSRIGRPRQIYTGVER 421

Query: 430 KLVPREER 437
VP EER
Sbjct: 422 DFVPVEER 429

>tr:Q7U122 [Q7U122] PROBABLE CITRATE SYNTHASE I GLTA2 (EC
2.3.3.1).>gp:BX248337_9 [BX248337] PROBABLE CITRATE
SYNTHASE I GLTA2 [Mycobacterium bovis AF2122/97]
Length = 431

▲ Top

Score = 535 bits (1377), Expect = e-150
Identities = 264/432 (61%), Positives = 326/432 (75%), Gaps = 2/432 (0%)

Query: 7 VATDNNAKAVLHYPGGFEMDII EASEGNNGVVLGKMLSETGLITFDPGYVSTGSTESKIT 66
+A ++ A L YPGGE ++ I+ A+EG +G+ LG +L++TG TFD G+ +T + +S IT
Sbjct: 1 MADTDDTATLRYPGGEIDLQIVHATEGADGIALGPLLAKTGHTTFDVGFAATAAKSSIT 60

Query: 67 YIDGDAGILRYRGYDIADLAENATFNEVSYLLINGELPTDELHKFNDEIRHHTLLDEDF 126
YIDGDAGILRYRGY I LAE +TF EV YLLI GELP D+L +F I+ HT+L ED
Sbjct: 61 YIDGDAGILRYRGYPIDQLAEKSTFIEVCYLLIYGELPDTDQLAQFTGRIQRHTMLHEDL 120

Query: 127 KSQFNVFPRDAHPMATLASSVNI LSTYYQDQLNPLDEAQLDKATVRLMAKVPMLAAYHR 186
K F+ FPR+AHPM L+S VN LS YYQD L+P+D Q++ +T+RL+AK+P +AAYA++
Sbjct: 121 KRFFDGFPRNAHPMPVLSSVSNALSAYYQDALDPMNGQVELSTIRLLAKLPTIAAYAYK 180

Query: 187 ARKGAPYMPDNLNARENFLRMMFGYPTEPYEIDPIMVKALDKLLILHADHEQNCSTST 246
G P++YPDNSL ENFLR+ FG+P EPY+ DP +V+ALD L ILHADHEQNCSTST
Sbjct: 181 KSVGQPFLLYPDNSLTLVENFLRLTFGFPAPYQADPEVVRALDMLFILHADHEQNCSTST 240

Query: 247 VRMIGSAQANMFVSIAGGINALSGPLHGGANQAVLEMLEDIKNNHGGDATAFMNKVKNKE 306
VR++GS++AN+F SI+GGINAL GPLHGGANQAVLEMLE I+++ G D + F+ KVKN+E
Sbjct: 241 VRLVGSSRANLFTSISGINALWGPLHGGANQAVLEMLEGIRDS-GDDVSEFVRKVKNRE 299

Query: 307 DGVRLMGFGHRVYKKNYDPRAAIVKETAHEILEHXXXXXXXXXA|K-LLEEIALADDYFISR 365
GV+LMGFGHRVYKKNYDPRA IVKE A +IL K LEE AL DDYFI R
Sbjct: 300 AGVKLMGFGHRVYKKNYDPRAIRIVKEQADKILAKLGGDSLLGIAKELEEALDDYFIER 359

Query: 366 KLYPNVDFYTGLIYRAMGFPTDFFTVLFAIGRLPGWIAHYREQLGAAGNKINRPRQVYTG 425
KLYPNVDFYTGLIYRA+GFPT FTVLFA+GRLPGWIAH+RE +KI RPRQ+YTG
Sbjct: 360 KLYPNVDFYTGLIYRALGFPTMFVLFALGRLPGWIAHWREMHDEGDSKIGRPRQIYTG 419

Query: 426 KESRKLVPREER 437
R V + R
Sbjct: 420 YAERDYVTIDAR 431

>sp:GISY_MYCTU [Q10530] Citrate synthase 1 (EC 2.3.3.1).>pir:E70782 [E70782] [▲Top](#)
probable gltA2 protein - Mycobacterium tuberculosis
(strain H37RV)>gp:AE000516_946 [AE000516] citrate
synthase [Mycobacterium tuberculosis
CDC1551]>gp:BX842574_319 [BX842574] PROBABLE CITRATE
SYNTHASE I GLTA2 [Mycobacterium tuberculosis H37Rv]
Length = 431

Score = 535 bits (1377), Expect = e-150
Identities = 264/432 (61%), Positives = 326/432 (75%), Gaps = 2/432 (0%)

Query: 7 VATDNNAVLHYPGGEFEMDIIEASEGNNGVVLGKMLSETGLITFDPGYVSTGSTESKIT 66
+A ++ A L YPGGE ++ I+ A+EG +G+ LG +L++TG TFD G+ +T + +S IT
Sbjct: 1 MADTDDTATLRYPGGEIDLQIVHATEGADGIALGPLLAKTGHTTFDVG FANTAAKSSIT 60

Query: 67 YIDGDAGILRYRGYDIADLAENATFNEVSYLLINGELPTDELHKFNDEIRHHTLLDEDF 126
YIDGDAGILRYRGY I LAE +TF EV YLLI GELP D+L +F I+ HT+L ED
Sbjct: 61 YIDGDAGILRYRGYPIDQLAEKSTFIEVCYLLIYGELPDTDQLAQFTGRIQRHTMLHEDL 120

Query: 127 KSQFNVFPRDAHPMATLASSVNIILSTYYQDQLNPLDEAQLDKATVRLMAKVPMLAAYHR 186
K F+ FPR+AHPM L+S VN LS YYQD L+P+D Q++ +T+RL+AK+P +AAYA++
Sbjct: 121 KRFFDGFPRNAHPMPVLSSVVNALSAYYQDALDPMNGQVELSTIRLLAKLPTIAAYAYK 180

Query: 187 ARKGAPYMPDNSLNARENFLRMMFGYPTEPYEIDPIMVKALDKLLILHADHEQNCSTST 246
G P++YPDNSL ENFLR+ FG+P EPY+ DP +V+ALD L ILHADHEQNCSTST
Sbjct: 181 KSVGQPFLLYPDNSLTLVENFLRLTFGFPAEPYQADPEVVRALDMLFILHADHEQNCSTST 240

Query: 247 VRMIGSAQANMFVSIAGGINALSGPLHGGANQAVLEMLEDIKNNHGGDATAFMNKVKNKE 306
VR++GS++AN+F SI+GGINAL GPLHGGANQAVLEMLE I+++ G D + F+ KVKN+E
Sbjct: 241 VRLVGSSRANLFTSISGINALWGPLHGGANQAVLEMLEGIRDS-GDDVSEFVRKVKNRE 299

Query: 307 DGVRLMGFGHRVYKNDPRAAIVKETAHEILEHXXXXXXXXXA I K-LEEIALADDYFISR 365
GV+LMGFGHRVYKNDPRA IVKE A +IL K LEE AL DDYFI R
Sbjct: 300 AGVKLMGFGHRVYKNDPRARIVKEQADKILAKLGGDSLLGIAKELEEAALTDYFIER 359

Query: 366 KLYPNVDFYTGLIYRANGFPTDFFTVLFAIGRLPGWIAHYREQLGAAGNKINRPRQVYTG 425
KLYPNVDFYTGLIYRA+GFPT FTVLFA+GRLPGWIAH+RE +KI RPRQ+YTG
Sbjct: 360 KLYPNVDFYTGLIYRALGFPTRMFTVLFALGRLPGWIAHREMHEGDSKIGRPRQIYTG 419

Query: 426 KESRKLVPREER 437
R V + R
Sbjct: 420 YTERDYVTIDAR 431

>tr:Q82CL5 [Q82CL5] Putative citrate synthase.>gpu:BA000030_5334 [BA000030] [▲Top](#)
putative citrate synthase [Streptomyces avermitilis
MA-4680]>gp:AP005042_136 [AP005042] putative citrate
synthase [Streptomyces avermitilis MA-4680]
Length = 429

Score = 533 bits (1372), Expect = e-150
Identities = 262/428 (61%), Positives = 325/428 (75%), Gaps = 2/428 (0%)

Query: 11 NNKAVLHYPGGEFEMDIIEASEGNNGVVLGKMLSETGLITFDPGYVSTGSTESKIT 70
+N VL Y GE+ +I+++ G+ G +GK+ ++TGL+T D GY +T + +S ITY+DG
Sbjct: 3 DNSVVLRYGDGEYTYPVIDSTVGDKGFDIGKLRAQTGLVTLDSGYGNTAAYKSAITYLDG 62

Query: 71 DAGILRYRGYDIADLAENATFNEVSYLLINGELPTDELHKFNDEIRHHTLLDEDFKSQF 130

+ GILRYRGY I LAE +TF EV+YLLINGELPT DEL F EI HTLL ED K+ +
Sbjct: 63 EQGILRYRGYPIEQLAERSTFLEVAYLLINGELPTVDELSTFKGEITQHTLLHEDVKNFY 122

Query: 131 NVFPRDAHPMATLASSVNI LSTYYQDQLNPLDEAQLDKATVRLMAKVPMLAAYHRARKG 190
FPRDAHPMA L+S V+ LST+YQD NP DE Q + +T+RL+AK+P +AAYA++ G
Sbjct: 123 RGFPRAHPMAMLSVVSALSTFYQDSHPFDEKQKNLSTIRLLAKLPTIAAYAYKKSIG 182

Query: 191 APYMPDNLNARENFLRMMFGYPTPEYIDPIMVKALDKLLILHADHEQNCSTSTVRMI 250
P++YP N L ENFLRM F P + Y++DP++V ALDKLLILHADHEQNCSTSTVR++
Sbjct: 183 HPFVYPRNDLGYVENFLRMTFSVPAQDYDLDPVVVSALDKLLILHADHEQNCSTSTVRLV 242

Query: 251 GSAQANMFVSIAGGINALSGPLHGGANQAVLEMLEDIKNNHGGDATAFMNKVKNKEDGVR 310
GS+QANMF SI+ GI+AL GPLHGGANQ+VLEMLE I+ + GGD F+ KVKNKEDGV+
Sbjct: 243 GSSQANMFASISAGISALWGPLHGGANQSVLEMLEGIQTS-GGDVDTFIRKVKNKEDGVK 301

Query: 311 LMGFGHRVYKNYDPRAAIVKETAHEILEH-XXXXXXXXXAIKLEEIALADDYFISRKLYP 369
LMGFGHRVYKN+DPRA I+K AH++L A+KLEE ALADDYF+ RKLYP
Sbjct: 302 LMGFGHRVYKNFDPRAKI IAAAHDVLSALGKSDELDDIALKLEEHALADDYFVERKLYP 361

Query: 370 NVDFYTGLIYRAMGFPTDFFTFLFAIGRLPGWIAHYREQLGAAGNKINRPRQVYTGKESR 429
NVDFYTGLIYRAMGFPT+ FTVLFA+GRLPGWIA + E + G++I RPRQ+YTG+ R
Sbjct: 362 NVDFYTGLIYRAMGFPTMFTVLFAIGRLPGWIAQWHEMIKEPGSRI GRPRQIYTGVEVL 421

Query: 430 KLVPREER 437
VP E R
Sbjct: 422 DFVPVEGR 429

Database: nr-aa: Non-redundant protein sequence database Release
05-01-04

Posted date: Jan 4, 2005 3:40 PM

Number of letters in database: 600,567,511

Number of sequences in database: 1,848,798

Lambda	K	H
0.319	0.137	0.399

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 527,441,587

Number of Sequences: 1848798

Number of extensions: 22621601

Number of successful extensions: 50691

Number of sequences better than 10.0: 10

Number of HSP's better than 10.0 without gapping: 665

Number of HSP's successfully gapped in prelim test: 43

Number of HSP's that attempted gapping in prelim test: 48255

Number of HSP's gapped (non-prelim): 739

length of query: 437

length of database: 600,567,511

effective HSP length: 128

effective length of query: 309

effective length of database: 363,921,367

effective search space: 112451702403

effective search space used: 112451702403

T: 11

A: 40

X1: 16 (7.4 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)

S1: 41 (21.7 bits)

S2: 75 (33.5 bits)

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